



BB-1163 US DIV Correct Sequence Listing

SEQUENCE LISTING

<110> Allen, Stephen M.
Hitz, William D.
Kinney, Anthony J.

<120> Plant Sugar Transport Proteins

<130> BB1163USDIV

<140> 10/051,902

<141> 2002-01-17

<150> 60/083,044

<151> 1998-04-24

<160> 30

<170> Microsoft Office 97

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<211> 2824

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| tccgcacccc | tcgctctcca | accccaacgc | gcggcggttg | taaaattcac | ctcagcgcg | 120 |
| actccagttt | ggccacctca | ccacccgccc | ccgctgttta | agaaggcccc | gcgcccgatc | 180 |
| ggggatcacg | aaccttggcc | gccgctgccg | gagtgggggc | gtagatttcc | ggcggccatg | 240 |
| gggggcgccg | tgatggtcgc | catcgcggcc | tctatcggca | acttgctgca | gggctgggac | 300 |
| aatgcgacaa | ttgctggagc | cgctcctgtac | ataaagaagg | aattcaacct | gcagagcgag | 360 |
| cctctgatcg | aaggcctcat | cgctcgccatg | ttcctcattg | gggcaacagt | catcacaaca | 420 |
| tctccggggc | caagggctga | ctgcggttgg | aggaggccca | tgctggtcgc | ctcggctgtc | 480 |
| ctctacttcg | tcagtgggct | ggtgatgctt | tgggcgccaa | ttgtgtacat | cttgctcctc | 540 |
| gcaaggctca | ttgatggggt | cggtatcggt | ttggcggtca | cacttgttcc | tctctacatc | 600 |
| tccgaaactg | caccgcacag | anattcttgg | ggctgntnga | acacgttgcc | gcagttcatt | 660 |
| ggggtcagng | gagggatgtt | cctctcctac | tgcatgggtg | ttgggatgtc | cctcatgccc | 720 |
| aaacctgatt | ggaggctcat | gcttgagggt | ctgtcgatcc | cgctacttat | ntactttgga | 780 |
| ctgactgtct | tctacttgcc | tgaatcacca | aggtggcttg | tnagcaaagg | aaggatggcg | 840 |
| gaggcgaaga | gagtgnatga | aaggctgcgg | ggaagagaag | atgtctcang | ggaganggct | 900 |
| cttctagttg | aaggtttggg | ggtcggtaaa | gatacacgta | tttnagagta | catcattgga | 960 |
| cctgccaccg | aggcagccga | tgatcttgta | actgacgggt | ataaggaaca | aatcacactt | 1020 |
| tatgggcctg | aagaaggcca | gtcatggatt | gctcgacctt | ctaagggacc | catcatgctt | 1080 |
| ggaagtgtgc | tttctcttgc | atctcgtcat | gggagcatgg | tgaaccagag | tgtaccctt | 1140 |
| atggatccga | ttgtgacact | ttttggtagt | gtccatgaga | atatgcctca | agctggagga | 1200 |
| agtatgagga | gcacattggt | tccaaacttt | ggaagtatgt | tcagtgtcac | agatcagcat | 1260 |
| gccaaaaatg | agcagtggga | tgaagagaat | cttcataggg | atgacgagga | gtacgcatct | 1320 |
| gatggtgcag | gaggtgacta | tgaggacaat | ctccatagcc | cattgctgtc | caggcaggca | 1380 |
| acaggtgcgg | aagggaagga | cattgtgcac | catggtcacc | gtggaagtgc | tttgagcatg | 1440 |
| agaaggcaaa | gcctcttagg | ggagggtgga | gatggtgtga | gcagcactga | tatcgggtgg | 1500 |
| ggatggcagc | ttgcttggaa | atggtcagag | aaggaagggt | agaatggtag | aaaggaagg | 1560 |
| ggtttcaaaa | gagtctactt | gcaccaagag | ggagttcctg | gctcaagaag | gggctcaatt | 1620 |
| gtttcacttc | ccggtggttg | cgatgttctt | gagggtagtg | agtttgtaca | tgctgctgct | 1680 |
| ttagtaagtc | agtcagcact | tttctcaaa | ggtcttgctg | aaccacgcat | gtcagatgct | 1740 |
| gccatgggtt | acccatctga | ggtagctgcc | aaaggttcac | ggttgaaaga | tttgtttgaa | 1800 |
| cctggagtga | ggcgtgccct | gttagtcggt | gttggaattc | agatccttca | acagtttgct | 1860 |
| ggaataaacg | gtgttctgta | ctatacccca | caaattcttg | agcaagctgg | tgtggcagtt | 1920 |
| attctttcca | aatttggtct | cagctcggca | tcagcatcca | tcttgatcag | ttctctcact | 1980 |
| accttactaa | tgcttccttg | cattggcttt | gccatgctgc | ttatggatct | ttccggaaga | 2040 |
| aggtttttgc | tgctaggcac | aattccaatc | ttgatagcat | ctctagtatt | cctggttgtg | 2100 |
| tccaatctaa | ttgatttggg | tacactagcc | catgctttgc | tctccaccat | cagtgttatc | 2160 |
| gtctactttc | gctgcttcgt | tatgggattt | ggtcccatcc | ccaacatttt | atgtgcagag | 2220 |
| atctttccaa | ccagggttcg | tggcctctgt | attgccattt | gtgcctttac | attctggatc | 2280 |
| ggagatatca | tcgtcaccta | cagccttcct | gtgatgctga | atgctatttg | actggcgggt | 2340 |
| gttttcagca | tatatgcagt | cgatgcttg | atttcctttg | tgttcgtctt | ccttaagggtc | 2400 |
| cctgagacaa | aggggatgcc | ccttgagggt | attaccgaat | tctttgcagt | tggtgcgaag | 2460 |
| caagcggctg | caaaagccta | atttcttttg | tacctttgtg | tgcaactatt | gcactgtaag | 2520 |
| ttagaaactt | gaagggtttt | caccaagaag | ctcggagaat | tactttggat | ttgtgtaaat | 2580 |
| gttaagggaa | cgaacatctg | ctcatgctcc | tcaaagcgtg | aaaaagagtc | cctcaatggc | 2640 |
| aaataggagt | cgtaaagttg | tcaatgtcat | ttaccatagt | ttttacctat | ttgtactgta | 2700 |

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ttataagtca agctattcaa cgctggttgt tgctagaaat ctttagaaca aagatgataa 2760
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 aaaa 2824

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 <213> Zea mays

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 Lys Lys Glu Phe Asn Leu Gln Ser Glu Pro Leu Ile Glu Gly Leu Ile
 35 40 45
 Val Ala Met Phe Leu Ile Gly Ala Thr Val Ile Thr Thr Ser Pro Gly
 50 55 60
 Pro Arg Ala Asp Cys Val Gly Arg Arg Pro Met Leu Val Ala Ser Ala

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| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Val | Leu | Tyr | Phe | Val | Ser | Gly | Leu | Val | Met | Leu | Trp | Ala | Pro | Ile | Val |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Tyr | Ile | Leu | Leu | Leu | Ala | Arg | Leu | Ile | Asp | Gly | Phe | Gly | Ile | Gly | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ala | Val | Thr | Leu | Val | Pro | Leu | Tyr | Ile | Ser | Glu | Thr | Ala | Pro | His | Arg |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Xaa | Ser | Trp | Gly | Xaa | Xaa | Asn | Thr | Leu | Pro | Gln | Phe | Ile | Gly | Val | Xaa |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Gly | Gly | Met | Phe | Leu | Ser | Tyr | Cys | Met | Val | Phe | Gly | Met | Ser | Leu | Met |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Pro | Lys | Pro | Asp | Trp | Arg | Leu | Met | Leu | Gly | Val | Leu | Ser | Ile | Pro | Ser |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Leu | Xaa | Tyr | Phe | Gly | Leu | Thr | Val | Phe | Tyr | Leu | Pro | Glu | Ser | Pro | Arg |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Trp | Leu | Val | Ser | Lys | Gly | Arg | Met | Ala | Glu | Ala | Lys | Arg | Val | Xaa | Gln |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Arg | Leu | Arg | Gly | Arg | Glu | Asp | Val | Ser | Xaa | Glu | Xaa | Ala | Leu | Leu | Val |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Glu | Gly | Leu | Gly | Val | Gly | Lys | Asp | Thr | Arg | Ile | Xaa | Glu | Tyr | Ile | Ile |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Gly | Pro | Ala | Thr | Glu | Ala | Ala | Asp | Asp | Leu | Val | Thr | Asp | Gly | Asp | Lys |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Glu | Gln | Ile | Thr | Leu | Tyr | Gly | Pro | Glu | Glu | Gly | Gln | Ser | Trp | Ile | Ala |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Arg | Pro | Ser | Lys | Gly | Pro | Ile | Met | Leu | Gly | Ser | Val | Leu | Ser | Leu | Ala |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Ser | Arg | His | Gly | Ser | Met | Val | Asn | Gln | Ser | Val | Pro | Leu | Met | Asp | Pro |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ile | Val | Thr | Leu | Phe | Gly | Ser | Val | His | Glu | Asn | Met | Pro | Gln | Ala | Gly |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Gly | Ser | Met | Arg | Ser | Thr | Leu | Phe | Pro | Asn | Phe | Gly | Ser | Met | Phe | Ser |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Val | Thr | Asp | Gln | His | Ala | Lys | Asn | Glu | Gln | Trp | Asp | Glu | Glu | Asn | Leu |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| His | Arg | Asp | Asp | Glu | Glu | Tyr | Ala | Ser | Asp | Gly | Ala | Gly | Gly | Asp | Tyr |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Glu | Asp | Asn | Leu | His | Ser | Pro | Leu | Leu | Ser | Arg | Gln | Ala | Thr | Gly | Ala |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Glu | Gly | Lys | Asp | Ile | Val | His | His | Gly | His | Arg | Gly | Ser | Ala | Leu | Ser |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Met | Arg | Arg | Gln | Ser | Leu | Leu | Gly | Glu | Gly | Gly | Asp | Gly | Val | Ser | Ser |

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| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--|
| | | | 405 | | | | | 410 | | | | | 415 | | | |
| Thr | Asp | Ile | Gly 420 | Gly | Gly | Trp | Gln | Leu 425 | Ala | Trp | Lys | Trp | Ser 430 | Glu | Lys | |
| Glu | Gly | Glu 435 | Asn | Gly | Arg | Lys | Glu 440 | Gly | Gly | Phe | Lys | Arg 445 | Val | Tyr | Leu | |
| His | Gln 450 | Glu | Gly | Val | Pro | Gly 455 | Ser | Arg | Arg | Gly | Ser 460 | Ile | Val | Ser | Leu | |
| Pro 465 | Gly | Gly | Gly | Asp | Val 470 | Leu | Glu | Gly | Ser | Glu 475 | Phe | Val | His | Ala | Ala 480 | |
| Ala | Leu | Val | Ser | Gln 485 | Ser | Ala | Leu | Phe | Ser 490 | Lys | Gly | Leu | Ala | Glu 495 | Pro | |
| Arg | Met | Ser | Asp 500 | Ala | Ala | Met | Val | His 505 | Pro | Ser | Glu | Val | Ala 510 | Ala | Lys | |
| Gly | Ser | Arg 515 | Trp | Lys | Asp | Leu | Phe 520 | Glu | Pro | Gly | Val | Arg 525 | Arg | Ala | Leu | |
| Leu | Val 530 | Gly | Val | Gly | Ile | Gln 535 | Ile | Leu | Gln | Gln | Phe 540 | Ala | Gly | Ile | Asn | |
| Gly 545 | Val | Leu | Tyr | Tyr | Thr 550 | Pro | Gln | Ile | Leu | Glu 555 | Gln | Ala | Gly | Val | Ala 560 | |
| Val | Ile | Leu | Ser | Lys 565 | Phe | Gly | Leu | Ser | Ser 570 | Ala | Ser | Ala | Ser | Ile 575 | Leu | |
| Ile | Ser | Ser | Leu 580 | Thr | Thr | Leu | Leu | Met 585 | Leu | Pro | Cys | Ile | Gly 590 | Phe | Ala | |
| Met | Leu | Leu 595 | Met | Asp | Leu | Ser | Gly 600 | Arg | Arg | Phe | Leu | Leu 605 | Leu | Gly | Thr | |
| Ile | Pro 610 | Ile | Leu | Ile | Ala | Ser 615 | Leu | Val | Ile | Leu | Val 620 | Val | Ser | Asn | Leu | |
| Ile 625 | Asp | Leu | Gly | Thr | Leu 630 | Ala | His | Ala | Leu | Leu 635 | Ser | Thr | Ile | Ser | Val 640 | |
| Ile | Val | Tyr | Phe | Cys 645 | Cys | Phe | Val | Met | Gly 650 | Phe | Gly | Pro | Ile | Pro 655 | Asn | |
| Ile | Leu | Cys | Ala 660 | Glu | Ile | Phe | Pro | Thr 665 | Arg | Val | Arg | Gly | Leu 670 | Cys | Ile | |
| Ala | Ile | Cys 675 | Ala | Phe | Thr | Phe | Trp 680 | Ile | Gly | Asp | Ile | Ile 685 | Val | Thr | Tyr | |
| Ser | Leu 690 | Pro | Val | Met | Leu | Asn 695 | Ala | Ile | Gly | Leu | Ala 700 | Gly | Val | Phe | Ser | |
| Ile 705 | Tyr | Ala | Val | Val | Cys 710 | Leu | Ile | Ser | Phe | Val 715 | Phe | Val | Phe | Leu | Lys 720 | |
| Val | Pro | Glu | Thr | Lys 725 | Gly | Met | Pro | Leu | Glu 730 | Val | Ile | Thr | Glu | Phe 735 | Phe | |
| Ala | Val | Gly | Ala | Lys | Gln | Ala | Ala | Ala | Lys | Ala | | | | | | |

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745

740

<210> 3
<211> 443
<212> DNA
<213> Oryza sativa

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tccagattcc cagccgcctc tcttcttggt aggggatccg aaatctcggg ggacgagaga 180
cttggtggtg atnattcgcc ggccatggcg ggcgccgtgc tggtcgccat cgcggcctcc 240
atcggaact tgctgcaggg ctgggataat gcaaccattg caggtgcggg actgtacatc 300
aagaaggaat tcaacttgca tagcgacccc cttatcgaag gtctgatcgt ggccatgtcg 360
ctcattgggg ccaccatcat caccgacgntc tctgcgagca ggtggctgac tcttttggtg 420
tggcggccca tgctnatacnc ttc 443

<210> 4
<211> 131
<212> PRT
<213> Oryza sativa

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<223> Xaa = any amino acid

<220>
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<222> (130)
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Glu Glu Leu Thr Pro Pro Pro Ser Ala Leu Asp Ser Leu Leu Gln Ile
1 5 10 15
Ser Pro Lys Ser Phe Pro Ile Trp Arg Glu Phe Pro Ile Tyr Leu Pro
20 25 30
His Leu Gly Val Pro Thr Ser Pro Ser Arg Phe Pro Ala Ala Ser Leu
35 40 45
Leu Val Arg Gly Ser Glu Ile Ser Val Asp Glu Arg Leu Gly Gly Asn

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50 55 60

Xaa Ser Pro Ala Met Ala Gly Ala Val Leu Val Ala Ile Ala Ala Ser
65 70 75 80

Ile Gly Asn Leu Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala
85 90 95

Val Leu Tyr Ile Lys Lys Glu Phe Asn Leu His Ser Asp Pro Leu Ile
100 105 110

Glu Gly Leu Ile Val Ala Met Ser Leu Ile Gly Ala Thr Ile Ile Thr
115 120 125

Thr Xaa Ser
130

<210> 5
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<212> DNA
<213> Oryza sativa

<400> 5

| | | | | | | |
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| ctcactgtcc | acagtcagtg | tcatactcta | cttctgcttc | tttgtcatgg | ggttcggggc | 120 |
| tattccaaac | attctctgtg | cagagatttt | cccgaccacc | gttcgtggca | tctgcatagc | 180 |
| catctgtgcc | ctaacattct | ggatcgggtga | tatcattgtg | acatacaccc | tccccgtgat | 240 |
| gctcaacgcc | attggactcg | ctggagtggt | tggaaatctac | gcagtgggtct | gcatactggc | 300 |
| tttcctgttt | gtcttcatga | agggtgccgga | gacaaagggc | atgcctcttg | aagtcatcac | 360 |
| cgagttcttc | tctgtcggag | caaagcaggc | caaggaggac | tagttgctcg | gatcaagtga | 420 |
| tcaatcagat | tgctgggtgt | aattttgttg | cttccaaatc | gcgctgcggg | ttaaacctgt | 480 |
| gatggatgct | ttgttaaaga | atcttggaag | agatcaaaat | gcagtgagcc | taaagagatg | 540 |
| atttggtgtg | acatcatgag | gctgaatcct | gtcgtagact | ggattttgga | gcttaggata | 600 |
| tgtagatcat | ctgttccttt | tggttttggtc | attttccatt | tgtgtttctt | tggaattctt | 660 |
| ctccctgtaa | ctagtgggtct | atcacagttg | tggtactggt | tttgccttac | tcttgagttt | 720 |
| gttttcttct | ctcggttgtg | agttctgaat | attagcatag | ccgagtacta | gttctgaatt | 780 |
| ggtttcctct | ctgctgaaca | tctttcattg | atgcttggat | ttcatcaaaa | aaaaaaaaaa | 840 |
| aaaactcgag | ggggagcccg | gtacacatct | | | | 870 |

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<211> 131
<212> PRT
<213> Oryza sativa

<400> 6

Val Leu Thr Leu Ile Leu Val Asn Ile Leu Asp Val Gly Thr Met Val
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His Ala Ser Leu Ser Thr Val Ser Val Ile Leu Tyr Phe Cys Phe Phe
20 25 30

Val Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe
35 40 45

Pro Thr Thr Val Arg Gly Ile Cys Ile Ala Ile Cys Ala Leu Thr Phe
50 55 60

Trp Ile Gly Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn
65 70 75 80

Ala Ile Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Val Val Cys Ile
85 90 95

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Leu Ala Phe Leu Phe Val Phe Met Lys Val Pro Glu Thr Lys Gly Met
100 105 110

Pro Leu Glu Val Ile Thr Glu Phe Phe Ser Val Gly Ala Lys Gln Ala
115 120 125

Lys Glu Asp
130

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<211> 2601
<212> DNA
<213> Glycine max

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tcccaactaa ctagcagttc cttgctgctg ctcccttctc accatatcgc agtaatgaaa 180
ggtgccgtcc ttggtgctat tgccgcttcc attggtaatt tcctccaagg atgggataat 240
gctaccatcg ccggggctaa tgggttacatt aagaaagacc ttgctttggg aacaactatg 300
gaaaggcttg tgggtgggcat gtccctgatt ggagcaacgg taatcaccac atgctctggt 360
cctatagcgg attggctcgg tcggcgaccc atgatgataa tctcatctgt gctctatttc 420
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cttgatggat ttgggattgg ctttgctgtg actcttgtcc cggctctatat atctgaaacg 540
gcgccgtctg aaataagggg gtcgttgaat acgcttcctc agttcagtgg ctctggagga 600
atgtttttgt cgtactgtat ggtttttggc atgtcattga gtcccgcgcc tagctggagg 660
ctcatgcttg gggttctgtc tattccttct ctcttgattt ttgcattgac ctttttttc 720
ttgcccagat ctccctcggg gctgggtcagc aaaggaagga tgctcgaggc taagaagggt 780
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gctgatggtc atgaacatgc aacagagaaa gataaaattc gattatatgg atcccaagca 960
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agcattcatg agaagctccc cgagacagga gcaagaggaa gcatgcgaag cactctgttt 1140
ccaaattttg gaagcatggt cagcactgct gagccgcatg ctaaaattga acaatgggat 1200
gaagaaagct tacaaaggga acgtgaggac tacatgtcag atgcaaccgg tggggactcc 1260
gatgataatt tgcacagtcc tttaattctca cgccaaacaa caagccttga aaaagactta 1320
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catgaggagg gagtttctgc atctcgtcgt ggatccattg tatcgattcc cgggtgaaggc 1560
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gcttttcata agtttatttg gaggaagata ttttgaaaca tatgggtttt tttttctttc 2520
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aaaaaaaaaa aaaaaaaaaa a 2601

<210> 8
<211> 737
<212> PRT

BB-1163 US DIV Correct Sequence Listing

<213> Glycine max

<400>

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  1      5      10     15

Leu  Gln  Gly  Trp  Asp  Asn  Ala  Thr  Ile  Ala  Gly  Ala  Asn  Gly  Tyr  Ile
      20     25     30

Lys  Lys  Asp  Leu  Ala  Leu  Gly  Thr  Thr  Met  Glu  Arg  Leu  Val  Val  Gly
      35     40     45

Met  Ser  Leu  Ile  Gly  Ala  Thr  Val  Ile  Thr  Thr  Cys  Ser  Gly  Pro  Ile
      50     55     60

Ala  Asp  Trp  Leu  Gly  Arg  Arg  Pro  Met  Met  Ile  Ile  Ser  Ser  Val  Leu
  65     70     75     80

Tyr  Phe  Leu  Gly  Gly  Leu  Val  Met  Leu  Trp  Ser  Pro  Asn  Val  Tyr  Val
      85     90     95

Leu  Cys  Leu  Ala  Arg  Leu  Leu  Asp  Gly  Phe  Gly  Ile  Gly  Leu  Ala  Val
      100    105    110

Thr  Leu  Val  Pro  Val  Tyr  Ile  Ser  Glu  Thr  Ala  Pro  Ser  Glu  Ile  Arg
      115    120    125

Gly  Ser  Leu  Asn  Thr  Leu  Pro  Gln  Phe  Ser  Gly  Ser  Gly  Gly  Met  Phe
      130    135    140

Leu  Ser  Tyr  Cys  Met  Val  Phe  Gly  Met  Ser  Leu  Ser  Pro  Ala  Pro  Ser
      145    150    155    160

Trp  Arg  Leu  Met  Leu  Gly  Val  Leu  Ser  Ile  Pro  Ser  Leu  Leu  Tyr  Phe
      165    170    175

Ala  Leu  Thr  Ile  Phe  Phe  Leu  Pro  Glu  Ser  Pro  Arg  Trp  Leu  Val  Ser
      180    185    190

Lys  Gly  Arg  Met  Leu  Glu  Ala  Lys  Lys  Val  Leu  Gln  Arg  Leu  Arg  Gly
      195    200    205

Arg  Glu  Asp  Val  Ser  Gly  Glu  Met  Ala  Leu  Leu  Val  Glu  Gly  Leu  Gly
      210    215    220

Ile  Gly  Gly  Asp  Thr  Ser  Ile  Glu  Glu  Tyr  Ile  Ile  Gly  Pro  Ala  Asp
      225    230    235    240

Asp  Val  Ala  Asp  Gly  His  Glu  His  Ala  Thr  Glu  Lys  Asp  Lys  Ile  Arg
      245    250    255

Leu  Tyr  Gly  Ser  Gln  Ala  Gly  Leu  Ser  Trp  Leu  Ser  Lys  Pro  Val  Thr
      260    265    270

Gly  Gln  Ser  Ser  Ile  Gly  Leu  Ala  Ser  His  His  Gly  Ser  Ile  Ile  Asn
      275    280    285

Gln  Ser  Met  Pro  Leu  Met  Asp  Pro  Leu  Val  Thr  Leu  Phe  Gly  Ser  Ile
      290    295    300

His  Glu  Lys  Leu  Pro  Glu  Thr  Gly  Ala  Arg  Gly  Ser  Met  Arg  Ser  Thr
      305    310    315    320

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BB-1163 US DIV Correct Sequence Listing

Leu Phe Pro Asn Phe Gly Ser Met Phe Ser Thr Ala Glu Pro His Ala
 325 330 335
 Lys Ile Glu Gln Trp Asp Glu Glu Ser Leu Gln Arg Glu Arg Glu Asp
 340 345 350
 Tyr Met Ser Asp Ala Thr Arg Gly Asp Ser Asp Asp Asn Leu His Ser
 355 360 365
 Pro Leu Ile Ser Arg Gln Thr Thr Ser Leu Glu Lys Asp Leu Pro Pro
 370 375 380
 Pro Pro Ser His Gly Ser Ile Leu Gly Ser Met Arg Arg His Ser Ser
 385 390 395 400
 Leu Met Gln Gly Ser Gly Glu Gln Gly Gly Ser Thr Gly Ile Gly Gly
 405 410 415
 Gly Trp Gln Leu Ala Trp Lys Trp Thr Asp Lys Gly Glu Asp Gly Lys
 420 425 430
 Gln Gln Gly Gly Phe Lys Arg Ile Tyr Leu His Glu Glu Gly Val Ser
 435 440 445
 Ala Ser Arg Arg Gly Ser Ile Val Ser Ile Pro Gly Glu Gly Glu Phe
 450 455 460
 Val Gln Ala Ala Ala Leu Val Ser Gln Pro Ala Leu Tyr Ser Lys Glu
 465 470 475 480
 Leu Ile Asp Gly His Pro Val Gly Pro Ala Met Val His Pro Ser Glu
 485 490 495
 Thr Ala Ser Lys Gly Pro Ser Trp Lys Ala Leu Leu Glu Pro Gly Val
 500 505 510
 Lys His Ala Leu Val Val Gly Val Gly Ile Gln Ile Leu Gln Gln Phe
 515 520 525
 Ser Gly Ile Asn Gly Val Leu Tyr Tyr Thr Pro Gln Ile Leu Glu Glu
 530 535 540
 Ala Gly Val Glu Val Leu Leu Ser Asp Ile Gly Ile Gly Ser Glu Ser
 545 550 555 560
 Ala Ser Phe Leu Ile Ser Ala Phe Thr Thr Phe Leu Met Leu Pro Cys
 565 570 575
 Ile Gly Val Ala Met Lys Leu Met Asp Val Ser Gly Arg Arg Gln Leu
 580 585 590
 Leu Leu Thr Thr Ile Pro Val Leu Ile Val Ser Leu Ile Ile Leu Val
 595 600 605
 Ile Gly Ser Leu Val Asn Phe Gly Asn Val Ala His Ala Ala Ile Ser
 610 615 620
 Thr Val Cys Val Val Val Tyr Phe Cys Cys Phe Val Met Gly Tyr Gly
 625 630 635 640
 Pro Ile Pro Asn Ile Leu Cys Ser Glu Ile Phe Pro Thr Arg Val Arg
 645 650 655

BB-1163 US DIV Correct Sequence Listing

Gly Leu Cys Ile Ala Ile Cys Ala Leu Val Phe Trp Ile Gly Asp Ile
660 665 670
Ile Ile Thr Tyr Ser Leu Pro Val Met Leu Gly Ser Leu Gly Leu Gly
675 680 685
Gly Val Phe Ala Ile Tyr Ala Val Val Cys Phe Ile Ser Trp Ile Phe
690 695 700
Val Phe Leu Lys Val Pro Glu Thr Lys Gly Met Pro Leu Glu Val Ile
705 710 715 720
Ser Glu Phe Phe Ser Val Gly Ala Lys Gln Ala Ala Ser Ala Lys Asn
725 730 735

Glu

<210> 9
<211> 1692
<212> DNA
<213> Glycine max

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gaagcatggc aaatccaagc agtctagtgg accctctagt gaccctcttt ggtagtgtac 180
atgagaagct cccagaaaca ggaagcacc tttttccaca ctttgggagt atgttcagt 240
ttgggggaaa tcagccaagg aatgaagatt gggatgagga aagcctagcc agagagggtg 300
atgattatgt ctctgatgct ggtgattctg atgacaattt gcagagtcca ttgatctcac 360
gtcaaacaac gagtctggat aaggacatac ctctcatgc ccatagtaac cttgcaagca 420
tgaggcaagg tagtctttta catggaaatt caggagaacc cactggtagt actgggattg 480
gtggtggttg gcagctagca tggaaatggt ctgaaagaga gggcccagat ggaaagaagg 540
aaggtggctt caagagaata tatttacacc aagatggttg ttctggatct agacgtgggt 600
ctgtggtttc actccctggc ggtgatttac caactgacag tgaggttgta caggctgctg 660
ctctggtgag tcagcctgcc ctttataatg aggaccttat gcgtcaacgg ccagttggac 720
cagctatgat tcatccctct gaaacaattg caaaagggcc aagttggagt gatctttttg 780
aacctggggg gaagcatgca ttgatttgtg ggggtgggaat gcaaattctt cagcagttct 840
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atcttctttc aagcctaggc cttggttcta cttcttcata ctttcttatt agtgcggtga 960
caaccttggt gatgcttcct tgtatagcca ttgccatgag gctcatggat atttcaggca 1020
gaaggacttt gctgctcagt acaatccccg tcctaatagc agctcttctc atattagtcc 1080
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ttccagaaac caagggcatg ccaactggaag tgatcattga gttcttctct gtcggagcaa 1440
aacagtttga cgatgccaag cacaactgac ccaaggacat gataaattca aagttttgac 1500
ggtaccttct aattattttc aatctacggc tgtttgaaat tttcccctct tttaaaattt 1560
tattttctat ttattctctc ttttccgtgg gttgagattg agaaacaaga aactttgttt 1620
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aaaaaaaaaa aa 1692

<210> 10
<211> 486
<212> PRT
<213> Glycine max

<400> 10
Asp Pro Ser Arg Glu Lys Asp Gln Ile Lys Leu Tyr Gly Pro Glu Gln
1 5 10 15

BB-1163 US DIV Correct Sequence Listing

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gln | Ser | Trp | Val | Ala | Arg | Pro | Val | Ala | Gly | Pro | Asn | Ser | Val | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Val | Ser | Arg | Lys | Gly | Ser | Met | Ala | Asn | Pro | Ser | Ser | Leu | Val | Asp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Pro | Leu | Val | Thr | Leu | Phe | Gly | Ser | Val | His | Glu | Lys | Leu | Pro | Glu | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Ser | Thr | Leu | Phe | Pro | His | Phe | Gly | Ser | Met | Phe | Ser | Val | Gly | Gly |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Asn | Gln | Pro | Arg | Asn | Glu | Asp | Trp | Asp | Glu | Glu | Ser | Leu | Ala | Arg | Glu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gly | Asp | Asp | Tyr | Val | Ser | Asp | Ala | Gly | Asp | Ser | Asp | Asp | Asn | Leu | Gln |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Pro | Leu | Ile | Ser | Arg | Gln | Thr | Thr | Ser | Leu | Asp | Lys | Asp | Ile | Pro |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Pro | His | Ala | His | Ser | Asn | Leu | Ala | Ser | Met | Arg | Gln | Gly | Ser | Leu | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| His | Gly | Asn | Ser | Gly | Glu | Pro | Thr | Gly | Ser | Thr | Gly | Ile | Gly | Gly | Gly |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Trp | Gln | Leu | Ala | Trp | Lys | Trp | Ser | Glu | Arg | Glu | Gly | Pro | Asp | Gly | Lys |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Lys | Glu | Gly | Gly | Phe | Lys | Arg | Ile | Tyr | Leu | His | Gln | Asp | Gly | Gly | Ser |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Gly | Ser | Arg | Arg | Gly | Ser | Val | Val | Ser | Leu | Pro | Gly | Gly | Asp | Leu | Pro |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Thr | Asp | Ser | Glu | Val | Val | Gln | Ala | Ala | Ala | Leu | Val | Ser | Gln | Pro | Ala |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Leu | Tyr | Asn | Glu | Asp | Leu | Met | Arg | Gln | Arg | Pro | Val | Gly | Pro | Ala | Met |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ile | His | Pro | Ser | Glu | Thr | Ile | Ala | Lys | Gly | Pro | Ser | Trp | Ser | Asp | Leu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Phe | Glu | Pro | Gly | Val | Lys | His | Ala | Leu | Ile | Val | Gly | Val | Gly | Met | Gln |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ile | Leu | Gln | Gln | Phe | Ser | Gly | Ile | Asn | Gly | Val | Leu | Tyr | Tyr | Thr | Pro |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Gln | Ile | Leu | Glu | Gln | Ala | Gly | Val | Gly | Tyr | Leu | Leu | Ser | Ser | Leu | Gly |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Leu | Gly | Ser | Thr | Ser | Ser | Ser | Phe | Leu | Ile | Ser | Ala | Val | Thr | Thr | Leu |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Leu | Met | Leu | Pro | Cys | Ile | Ala | Ile | Ala | Met | Arg | Leu | Met | Asp | Ile | Ser |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Gly | Arg | Arg | Thr | Leu | Leu | Leu | Ser | Thr | Ile | Pro | Val | Leu | Ile | Ala | Ala |
| | | | 340 | | | | | 345 | | | | | 350 | | |

BB-1163 US DIV Correct Sequence Listing

Leu Leu Ile Leu Val Leu Gly Ser Leu Val Asp Leu Gly Ser Thr Ala
355 360 365

Asn Ala Ser Ile Ser Thr Ile Ser Val Ile Val Tyr Phe Cys Phe Phe
370 375 380

Val Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe
385 390 395 400

Pro Thr Arg Val Arg Gly Leu Cys Ile Ala Ile Cys Ala Leu Thr Phe
405 410 415

Trp Ile Cys Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn
420 425 430

Ser Val Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Val Val Cys Phe
435 440 445

Ile Ala Trp Val Phe Val Phe Leu Lys Val Pro Glu Thr Lys Gly Met
450 455 460

Pro Leu Glu Val Ile Ile Glu Phe Phe Ser Val Gly Ala Lys Gln Phe
465 470 475 480

Asp Asp Ala Lys His Asn
485

<210> 11
<211> 510
<212> DNA
<213> Triticum aestivum

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<223> n = a, c, g or t

<220>
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<222> (434)
<223> n = a, c, g or t

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BB-1163 US DIV Correct Sequence Listing

<221> unsure
 <222> (498)
 <223> n = a, c, g or t

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 ctcggttctg atctaccgca ccacaccacc acaccacacc aggggcctgc cgcttcttgg 120
 gcttctccat ctcactctct tgggttggtc tctactagag aggcgcagct gcagggatcc 180
 ttggtggaga ggagggaaga agatgtcggg tgctgcactg gtcgcgattg cggcttccat 240
 tggcaatctg ctgcaggggt gggacaatgc caccatcgct ggtgctgttc tgtacatcaa 300
 gaaggaattc cagctcgaaa ataatccgac tgtggagggg ctcatcgtgg catgtcctca 360
 tcgggtgcaa catcatcaca cattctccgg gccagtatca aactgggttg ccgggcccta 420
 ngccatctcc ttgntttcaa ntcccaaggg ctaatcanct aggcaccaat gtcaatgtgc 480
 gcnccggaac cnttcaangg ttggaacgtt 510

<210> 12
 <211> 117
 <212> PRT
 <213> Triticum aestivum

<400> 12
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 Arg Arg Leu Arg Ser Val Leu Ile Tyr Arg Thr Thr Pro Pro His His
 20 25 30
 Thr Arg Gly Leu Pro Leu Leu Gly Leu Leu His Leu Ile Ser Leu Val
 35 40 45
 Gly Ser Leu Leu Glu Arg Arg Ser Cys Arg Asp Pro Trp Trp Arg Gly
 50 55 60
 Gly Lys Lys Met Ser Gly Ala Ala Leu Val Ala Ile Ala Ala Ser Ile
 65 70 75 80
 Gly Asn Leu Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val
 85 90 95
 Leu Tyr Ile Lys Lys Glu Phe Gln Leu Glu Asn Asn Pro Thr Val Glu
 100 105 110
 Gly Leu Ile Val Ala
 115

<210> 13
 <211> 1487
 <212> DNA
 <213> Triticum aestivum

<400> 13
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 tcgcatggaa atggtcggag cgacaaggcg aggatggcaa gaaggaagga ggcttcaaaa 120
 gaatctactt gcaccaagag ggggtggccg actcaagaag gggctctgtt gtttcacttc 180
 ctggtggggg tgatgccacg caagggggca gtgggtttat acatgctgct gctttggtta 240
 gccactcggc tctttactcc aaggatctta tggaagagcg tatggcggcc ggtccagcca 300
 tgattcatcc attggaggca gctcccaaag gttcaatctg gaaagatctg tttgaacctg 360
 gtgtgaggcg tgcattgttc gtcgggtgtt gaattcagat gcttcagcag tttgctggaa 420
 taaatggagt tctctactat actcctcaaa ttctggagca agctggtgtg gctgttcttc 480
 tttccaatct tggcctcagt tcagcatcag catccatctt gatcagttct ctcaccacct 540
 tactcatgct cccaagcatt ggtgtagcca tgagacttat ggatatatct ggaagaaggt 600
 ttctgctact gggcacaatt cccatcttga tagcatccct aattgttttg ggtgtggtca 660
 atgttatcaa cttgagtacg gtgccccacg ctgtgctctc cacagttagc gtcattgtct 720

BB-1163 US DIV Correct Sequence Listing

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|------|
| acttctgctg | ctttgtcatg | ggctttggcc | cgatcccca | cattctatgt | gcagagattt | 780 |
| tccccaccag | agtccgtggt | gtctgcatcg | ctatttgcg | cctcacattc | tggatttgtg | 840 |
| acattattgt | tacctacagc | ctgcctgtga | tgctgaatgc | tattgggtcta | gcgggtgtct | 900 |
| ttggtatata | tgcagtcggt | tgctgcattg | cctttgtgtt | cgtctaccta | aaggtcccag | 960 |
| agacaaaggg | catgcccctc | gagggtcatca | ccgagttctt | tgcggttggg | gcgaagcaag | 1020 |
| cgcaggccac | cattgcctga | ttcatcatgg | agctttgttt | tcagtttgca | cactgcggtc | 1080 |
| tgcgctgaaa | attgcaaatt | ggacgggtcc | tcgtgaggaa | cggaaaaact | tttgagttgt | 1140 |
| aaatgagaca | gctacccaaa | gagctcatca | cgaggaacgg | gaagctgtaa | aagtaggagg | 1200 |
| atctcatgcc | cccatttcat | cgtctattat | tgcttattag | tactgtactg | taatcgtcac | 1260 |
| tagttgctgt | agggttgttc | aacttgctaa | tctgattctg | aactaccatg | ctgatgtccg | 1320 |
| aaataaagaa | aaagcatggt | tttttttgtg | tcaacttgca | aactttcttt | taaacattgt | 1380 |
| gcaatgtatt | gtaaatttct | ttatcaactt | ccctcgattc | agagagaagc | acttgtttgt | 1440 |
| aagtcatgaa | agatttttct | cgacaaaaaa | aaaaaaaaaa | aaaaaaa | | 1487 |

<210> 14
 <211> 345
 <212> PRT
 <213> Triticum aestivum

<400> 14
 Ser Trp Lys Glu Gly Gly Glu Ala Val Ser Ser Thr Gly Ile Gly Gly
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 Gly Trp Gln Leu Ala Trp Lys Trp Ser Glu Arg Gln Gly Glu Asp Gly
 20 25 30
 Lys Lys Glu Gly Gly Phe Lys Arg Ile Tyr Leu His Gln Glu Gly Val
 35 40 45
 Ala Asp Ser Arg Arg Gly Ser Val Val Ser Leu Pro Gly Gly Gly Asp
 50 55 60
 Ala Thr Gln Gly Gly Ser Gly Phe Ile His Ala Ala Ala Leu Val Ser
 65 70 75 80
 His Ser Ala Leu Tyr Ser Lys Asp Leu Met Glu Glu Arg Met Ala Ala
 85 90 95
 Gly Pro Ala Met Ile His Pro Leu Glu Ala Ala Pro Lys Gly Ser Ile
 100 105 110
 Trp Lys Asp Leu Phe Glu Pro Gly Val Arg Arg Ala Leu Phe Val Gly
 115 120 125
 Val Gly Ile Gln Met Leu Gln Gln Phe Ala Gly Ile Asn Gly Val Leu
 130 135 140
 Tyr Tyr Thr Pro Gln Ile Leu Glu Gln Ala Gly Val Ala Val Leu Leu
 145 150 155 160
 Ser Asn Leu Gly Leu Ser Ser Ala Ser Ala Ser Ile Leu Ile Ser Ser
 165 170 175
 Leu Thr Thr Leu Leu Met Leu Pro Ser Ile Gly Val Ala Met Arg Leu
 180 185 190
 Met Asp Ile Ser Gly Arg Arg Phe Leu Leu Leu Gly Thr Ile Pro Ile
 195 200 205
 Leu Ile Ala Ser Leu Ile Val Leu Gly Val Val Asn Val Ile Asn Leu
 210 215 220
 Ser Thr Val Pro His Ala Val Leu Ser Thr Val Ser Val Ile Val Tyr

BB-1163 US DIV Correct Sequence Listing

<400>
Glu 1 Pro Gly 16 Val Lys 5 His Ala Leu Phe Val 10 Gly Ile Gly Leu Gln 15 Ile
Leu Gln Gln Phe 20 Ala Gly Ile Asn 25 Val Leu Tyr Tyr 30 Thr Pro Gln
Ile Leu Glu 35 Gln Ala Gly Val Gly 40 Val Leu Leu Ser Asn 45 Ile Gly Leu
Ser Ser Ser Ser Ala Ser Ile Leu Ile Ser Ala Leu Thr Thr Leu Leu

BB-1163 US DIV Correct Sequence Listing

50

55

60

Met Leu Pro Ser Ile Gly Ile Ala Met Arg Leu Met Asp Met Ser Gly
65 70 75 80
Arg Arg Phe Leu Leu Ser Thr Ile Pro Val Leu Ile Val Ala Leu
85 90 95
Ala Val Leu Val Leu Val Asn Val Leu Asp Val Gly Thr Met Val His
100 105 110
Ala Ala Leu Ser Thr Ile Ser Val Ile Val Tyr Phe Cys Phe Phe Val
115 120 125
Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe Pro
130 135 140
Thr Ser Val Arg Gly Ile Cys Ile Ala Ile Cys Ala Leu Thr Phe Trp
145 150 155 160
Ile Gly Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn Ala
165 170 175
Ile Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Ile Val Cys Val Leu
180 185 190
Ala Phe Val Phe Val Tyr Met Lys Val Pro Glu Thr Lys Gly Met Pro
195 200 205
Leu Glu Val Ile Thr Glu Phe Phe Ser Val Gly Ala Lys Gln Gly Lys
210 215 220

Glu Ala Thr Asp
225

<210> 17
<211> 615
<212> DNA
<213> Zea mays

<220>
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<222> (149)
<223> n = a, c, g or t

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<222> (271)
<223> n = a, c, g or t

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<222> (304)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (334)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (357)

BB-1163 US DIV Correct Sequence Listing

<223> n = a, c, g or t

<220>

<221> unsure

<222> (476)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (599)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (602)

<223> n = a, c, g or t

<400> 17

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| gaaacgaact | ctcttgagta | ccacaaaaaa | aaacattggc | attctctgta | gtagagcaca | 60 |
| gagcgaaccg | tcaacgatgg | cttccgctcc | gctgccggcg | gccatcgagc | ccgggaagaa | 120 |
| aggcaacgtc | aagttcgcct | tcgcctgcnc | catcctcgcc | tcaatgacct | ccatccttct | 180 |
| cggctatgat | atcggagtga | tgagcggcgc | gtcgttgtag | atcaagaagg | acctgaaaat | 240 |
| cagcgacgtg | aagctggaga | tcctgatggg | nacctcaac | gtgtactcgc | tcatcggctc | 300 |
| gttngcggca | gggcggacgt | ccgactggat | cggncgccgt | acaccatcgt | gttcgcngcg | 360 |
| gtgatcttct | tcgcggggcg | ttcctcatgg | gcttcgccgt | gaactactgg | atgctcatgt | 420 |
| tcgggcgctt | cgtggccggg | atcggcgtgg | gctacgcgct | catgatcgca | accgtntaca | 480 |
| cggccgaagt | gtccccgcat | cggcccgcgg | cttcctgacg | tcgttcccgg | aggtgttcat | 540 |
| cacttcggca | tcctctaggt | acgtgtcaat | aaggcttttc | cgcttccggt | cgctggatng | 600 |
| cnctaattgtc | ggcat | | | | | 615 |

<210> 18

<211> 167

<212> PRT

<213> Zea mays

<220>

<221> UNSURE

<222> (34)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (85)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (98)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (112)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (151)

<223> Xaa = any amino acid

<400> 18

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Ala | Gln | Ser | Glu | Pro | Ser | Thr | Met | Ala | Ser | Ala | Pro | Leu | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

BB-1163 US DIV Correct Sequence Listing

Ala Ala Ile Glu Pro Gly Lys Lys Gly Asn Val Lys Phe Ala Phe Ala
20 25 30
Cys Xaa Ile Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp Ile
35 40 45
Gly Val Met Ser Gly Ala Ser Leu Tyr Ile Lys Lys Asp Leu Lys Ile
50 55 60
Ser Asp Val Lys Leu Glu Ile Leu Met Gly Ile Leu Asn Val Tyr Ser
65 70 75 80
Leu Ile Gly Ser Xaa Ala Ala Gly Arg Thr Ser Asp Trp Ile Gly Arg
85 90 95
Arg Xaa Thr Ile Val Phe Ala Ala Val Ile Phe Phe Ala Gly Ala Xaa
100 105 110
Leu Met Gly Phe Ala Val Asn Tyr Trp Met Leu Met Phe Gly Arg Phe
115 120 125
Val Ala Gly Ile Gly Val Gly Tyr Ala Leu Met Ile Ala Thr Val Tyr
130 135 140
Thr Ala Glu Val Ser Pro Xaa Ser Ala Arg Gly Phe Leu Thr Ser Phe
145 150 155 160
Pro Glu Val Phe Ile Thr Ser
165

<210> 19
<211> 1914
<212> DNA
<213> Zea mays

<400> 19
gcacgaggga cgccaccta tctctaaccg gagatcaaag aagtagccgt taacgatggc 60
ttccgacgag ctcgcaaagg ccgtcgagcc caggaagaag ggcaacgtca agtatgcctc 120
catatgtgcc atcctggcct ccatggcctc tgtcatcctt ggctatgaca ttgggggtgat 180
gagtggagcg gccatgtaca tcaagaagga cctgaatata acggacgtgc agctggagat 240
cctgatcggg atcctcagtc tctactcgtt gttcggatcc ttcgctggcg cgcggacgtc 300
cgacaggatc gggcgccgct tgaccgtcgt gttcggcgtt gtcattctct tcgtgggctc 360
gttgctcatg gggttcgccc tcaactacgg catgctcatg gcgggcccgt tcgtggccgg 420
agtcggtgtg ggctacgggg gcatgatcgc gcccggtgtac acggccgaga tctcgcctgc 480
ggcgtcccgt ggcttcctga ccaccttccc ggaggtgttc atcaacatcg gcatcctgct 540
tggctacctg tccaacttcg cggttcgccc cctcccgtc cacctcggct ggcgcgatcat 600
gctcgccatt ggcgagttc cgctccggcct gctcgcgctc ctggtgttct gcatgcccga 660
gtcgcctcgg tggctgggtc tgaaggggcg cctcgcggac gccagggtcg tgctagagaa 720
gacctctgcc acgccagagg aggccggcga gcggctggcc gacatcaagg ccgcggcggg 780
gattccgaag ggcctcgacg gggacgtagt caccgtaccc ggcaaggagc aaggcggcgg 840
tgagttgcag gtgtggaaga agctcatcct gtcccgcacc ccggctgtcc gacgcatact 900
gctctcggcc gtgggtctcc acttcttcca gcaggcttct ggcagcgact ccgtcgtcca 960
gtacagcgcc cgcctgttca agagcgcggg gatcaccgac gacaacaagc tcctgggctg 1020
cacctgcgcg gtgggcgtga ccaagacgtt cttcatcctg gtggccacgt tcctgctgga 1080
ccgcgcgggg cgtcggcctc tgctgctgat cagcacgggc gggatgattg tctcgtcat 1140
ctgcctcggg tcggggctca ccgtcgcggg gcatcacccg gacaccaagg tcgcgtgggc 1200
cgtcgcccct tgcatcgcgt caaccctgtc ctacatcgcc ttcttctcca tcggcctcgg 1260
gcccatacag ggcgtgtaca cctcggaat attcccgtg caggtgcgcg cgctgggctt 1320
cgcggtgggt gtggcgagca accgcgtcac cagcgccgtc atctccatga ccttcctgtc 1380
cctctccaag gccatcacca tcggcggcag cttcttctc tactccggca tcgccgcggt 1440
cgcttgggtt ttcttcttca cgtgcctccc ggagacacgc ggccggacgc tggaggagat 1500
gggcaagctg ttcggcatgc cagacacggg catggctgaa gaagcagaag acgccgcagc 1560

BB-1163 US DIV Correct Sequence Listing

| | | | | | | |
|------------|-------------|-------------|-------------|------------|-------------|------|
| caaggagaag | gtggtggaac | tgcctagcag | caagtaggtg | gctatcccag | agcacagggtc | 1620 |
| aagtgaagta | gatggacaag | atcattgtct | tttcaactaa | ttagatgggc | aagaataact | 1680 |
| aagactgccc | tatgagggtgt | cgtgggttcaa | ccagagatca | ttctgctcct | tttcttttcc | 1740 |
| cttccttttt | cgagtaccat | tcccattcgt | cgtgggtcagt | acgatgttgg | gtcgttggga | 1800 |
| gttagtggtg | tcagagtccg | cgtgtgcttt | gcaagccagg | gctgaaccca | caatcatcag | 1860 |
| taacaaaaat | tcttccgttt | gctttgcaag | ccaaaaaaaa | aaaaaaaaaa | aaaa | 1914 |

<210> 20
 <211> 513
 <212> PRT
 <213> Zea mays

<400> 20
 Met Ala Ser Asp Glu Leu Ala Lys Ala Val Glu Pro Arg Lys Lys Gly
 1 5 10 15
 Asn Val Lys Tyr Ala Ser Ile Cys Ala Ile Leu Ala Ser Met Ala Ser
 20 25 30
 Val Ile Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala Ala Met Tyr
 35 40 45
 Ile Lys Lys Asp Leu Asn Ile Thr Asp Val Gln Leu Glu Ile Leu Ile
 50 55 60
 Gly Ile Leu Ser Leu Tyr Ser Leu Phe Gly Ser Phe Ala Gly Ala Arg
 65 70 75 80
 Thr Ser Asp Arg Ile Gly Arg Arg Leu Thr Val Val Phe Ala Ala Val
 85 90 95
 Ile Phe Phe Val Gly Ser Leu Leu Met Gly Phe Ala Val Asn Tyr Gly
 100 105 110
 Met Leu Met Ala Gly Arg Phe Val Ala Gly Val Gly Val Gly Tyr Gly
 115 120 125
 Gly Met Ile Ala Pro Val Tyr Thr Ala Glu Ile Ser Pro Ala Ala Ser
 130 135 140
 Arg Gly Phe Leu Thr Thr Phe Pro Glu Val Phe Ile Asn Ile Gly Ile
 145 150 155 160
 Leu Leu Gly Tyr Leu Ser Asn Phe Ala Phe Ala Arg Leu Pro Leu His
 165 170 175
 Leu Gly Trp Arg Val Met Leu Ala Ile Gly Ala Val Pro Ser Gly Leu
 180 185 190
 Leu Ala Leu Leu Val Phe Cys Met Pro Glu Ser Pro Arg Trp Leu Val
 195 200 205
 Leu Lys Gly Arg Leu Ala Asp Ala Arg Ala Val Leu Glu Lys Thr Ser
 210 215 220
 Ala Thr Pro Glu Glu Ala Ala Glu Arg Leu Ala Asp Ile Lys Ala Ala
 225 230 235 240
 Ala Gly Ile Pro Lys Gly Leu Asp Gly Asp Val Val Thr Val Pro Gly
 245 250 255
 Lys Glu Gln Gly Gly Gly Glu Leu Gln Val Trp Lys Lys Leu Ile Leu
 260 265 270

BB-1163 US DIV Correct Sequence Listing

Ser Pro Thr Pro Ala Val Arg Arg Ile Leu Leu Ser Ala Val Gly Leu
275 280 285
His Phe Phe Gln Gln Ala Ser Gly Ser Asp Ser Val Val Gln Tyr Ser
290 295 300
Ala Arg Leu Phe Lys Ser Ala Gly Ile Thr Asp Asp Asn Lys Leu Leu
305 310 315
Gly Val Thr Cys Ala Val Gly Val Thr Lys Thr Phe Phe Ile Leu Val
325 330 335
Ala Thr Phe Leu Leu Asp Arg Ala Gly Arg Arg Pro Leu Leu Leu Ile
340 345 350
Ser Thr Gly Gly Met Ile Val Ser Leu Ile Cys Leu Gly Ser Gly Leu
355 360 365
Thr Val Ala Gly His His Pro Asp Thr Lys Val Ala Trp Ala Val Ala
370 375 380
Leu Cys Ile Ala Ser Thr Leu Ser Tyr Ile Ala Phe Phe Ser Ile Gly
385 390 395 400
Leu Gly Pro Ile Thr Gly Val Tyr Thr Ser Glu Ile Phe Pro Leu Gln
405 410 415
Val Arg Ala Leu Gly Phe Ala Val Gly Val Ala Ser Asn Arg Val Thr
420 425 430
Ser Ala Val Ile Ser Met Thr Phe Leu Ser Leu Ser Lys Ala Ile Thr
435 440 445
Ile Gly Gly Ser Phe Phe Leu Tyr Ser Gly Ile Ala Ala Val Ala Trp
450 455 460
Val Phe Phe Phe Thr Cys Leu Pro Glu Thr Arg Gly Arg Thr Leu Glu
465 470 475 480
Glu Met Gly Lys Leu Phe Gly Met Pro Asp Thr Gly Met Ala Glu Glu
485 490 495
Ala Glu Asp Ala Ala Ala Lys Glu Lys Val Val Glu Leu Pro Ser Ser
500 505 510

Lys

<210> 21
<211> 2017
<212> DNA
<213> Oryza sativa

<400> 21
cttacatgta agctcgtgcc ggcacgagct tacactcgac cgccactact gtacacggcc 60
cagagcgagc ctcctcctcc tctgcaccac cggagatggc ttccgccgcg ctgccggagg 120
ccgtcgcgcc gaagaagaag ggcaacgtcc gggtcgcctt cgcctgcgcc atcctcgcct 180
ccatgacctc catcctcctc ggctacgata tcgggggtgat gagcggggcg tcgctgtaca 240
tcaagaagga cttcaacatc agtgacggga aggtggaggt tctcatgggc atactgaacc 300
tctactcgct catcggctcc ttcgcggcgg ggcggacgtc ggactggatc ggccggcggt 360
acaccatcgt gttcgccgcc gtcataattct tcgcgggggs gttcctcatg gggttcgccg 420
tcaactacgc catgctcatg ttcggccgct tcgtggcccg catcggcgtg ggctacgcgc 480

BB-1163 US DIV Correct Sequence Listing

| | | | | | | |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| tcatgatcgc | gccggtgtac | accgccgagg | tgtcgccggc | gtcggcgcggt | ggcttcctga | 540 |
| cgtcgttccc | ggaggtgttc | atcaacttcg | gcatacctgct | cgggtacgtc | tcgaactatg | 600 |
| ctttctcccg | cttgccgctg | aacctcgggt | ggcgcatcat | gctcggcatc | ggcgcgggcg | 660 |
| cgtccgtgct | gctcgcgctc | atggtgctcg | gcatgccgga | gtcgccgcgg | tggctggtca | 720 |
| tgaagggacg | cctcgcggac | gccaaaggtgg | tgctggagaa | gacctccgac | acggcgggagg | 780 |
| aggccgcgga | gcgcctggcc | gacatcaagg | ccgccgccgg | catccctgag | gagctcgacg | 840 |
| gcgacgtggt | gaccgtcccc | aagagagggg | gcggaaacga | gaagcgggtg | tggaggagc | 900 |
| tcatcctgtc | cccgaccccc | gccatgcggc | gcatacctgct | gtccgggatac | ggcatccact | 960 |
| tcttccagca | tgcgttgggc | attcactccg | tcgtcttcta | cagccctctc | gtgttcaaga | 1020 |
| gccccggatt | aacgaacgac | aaacacttct | tgggcaccac | ttggccgttc | ggtgtcacca | 1080 |
| agaggctttt | catcttgttg | gcgactttct | tcatcgacgg | cgtcgggcgg | cggccgctgt | 1140 |
| tgctgggcag | cacgggcggg | ataatcctct | ccctcatcgg | cctcggcgcc | gggctcaccg | 1200 |
| tcgtcggcca | gcacccccgac | gccaaagatac | cttggggccat | cggcctaagc | atcgccctcca | 1260 |
| ccctcgccta | cgtcgccttc | ttctccatcg | gccttgggccc | catcacgtgg | gtgtacagct | 1320 |
| cggagatctt | cccgcctccag | gtgcgcgcgc | tgggctgctc | gctcggcgctc | gccgccaacc | 1380 |
| gcgtcaccag | cggcgtcatc | tccatgacct | tcctgtcgct | gtccaaggcc | atcaccatcg | 1440 |
| gcggcagctt | cttcctctac | tccggcatcg | ccgcgctcgc | ctgggtgttc | ttctacacct | 1500 |
| acctcccga | gacccgcggc | cggacgctgg | aggagatgag | caagctgttc | ggcgacacgg | 1560 |
| ccgccgcctc | ggaatcagac | gagccagcca | aggagaagaa | gaaggtggaa | atggccgcca | 1620 |
| ctaactgata | aaactaaccg | caaaatcacc | aaatcctaag | ggttttcttg | caaaaacgtg | 1680 |
| tgctgtactg | gctagctagc | aagtagtagc | agcaacgtgg | gaagattcgc | tgatccggcg | 1740 |
| ttgctggaga | gcgacggccg | gcgacgacaa | agctgagctc | cagctcgaga | cttcttaaaa | 1800 |
| tcatcttcaa | gtacatggat | tttattttgc | tctttgcttt | gtccgtaaaa | gttgtactat | 1860 |
| gcgatgaaga | ataccagtat | gtagcaaggc | tgaggttgtg | tgtagctact | agaagtgtca | 1920 |
| gtcacgttgt | tcttgtaaga | aatgtttaac | tgtaatttaa | gcagtattgt | tgcagtaatc | 1980 |
| aaaaaaaaaa | aaaaaaaaaa | aaaaaaaaaa | aaaaaaa | | | 2017 |

<210> 22
 <211> 510
 <212> PRT
 <213> Oryza sativa

<220>
 <221> UNSURE
 <222> (102)
 <223> Xaa = any amino acid

<400> 22
 Met Ala Ser Ala Ala Leu Pro Glu Ala Val Ala Pro Lys Lys Lys Gly
 1 5 10 15
 Asn Val Arg Phe Ala Phe Ala Cys Ala Ile Leu Ala Ser Met Thr Ser
 20 25 30
 Ile Leu Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala Ser Leu Tyr
 35 40 45
 Ile Lys Lys Asp Phe Asn Ile Ser Asp Gly Lys Val Glu Val Leu Met
 50 55 60
 Gly Ile Leu Asn Leu Tyr Ser Leu Ile Gly Ser Phe Ala Ala Gly Arg
 65 70 75 80
 Thr Ser Asp Trp Ile Gly Arg Arg Tyr Thr Ile Val Phe Ala Ala Val
 85 90 95
 Ile Phe Phe Ala Gly Xaa Phe Leu Met Gly Phe Ala Val Asn Tyr Ala
 100 105 110
 Met Leu Met Phe Gly Arg Phe Val Ala Gly Ile Gly Val Gly Tyr Ala
 115 120 125
 Leu Met Ile Ala Pro Val Tyr Thr Ala Glu Val Ser Pro Ala Ser Ala

BB-1163 US DIV Correct Sequence Listing

| 130 | 135 | 140 | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--|
| Arg 145 | Gly | Phe | Leu | Thr | Ser 150 | Phe | Pro | Glu | Val | Phe 155 | Ile | Asn | Phe | Gly | Ile 160 | |
| Leu | Leu | Gly | Tyr | Val 165 | Ser | Asn | Tyr | Ala | Phe 170 | Ser | Arg | Leu | Pro | Leu 175 | Asn | |
| Leu | Gly | Trp | Arg 180 | Ile | Met | Leu | Gly | Ile 185 | Gly | Ala | Ala | Pro | Ser 190 | Val | Leu | |
| Leu | Ala | Leu 195 | Met | Val | Leu | Gly | Met 200 | Pro | Glu | Ser | Pro | Arg 205 | Trp | Leu | Val | |
| Met | Lys 210 | Gly | Arg | Leu | Ala | Asp 215 | Ala | Lys | Val | Val | Leu 220 | Glu | Lys | Thr | Ser | |
| Asp 225 | Thr | Ala | Glu | Glu | Ala 230 | Ala | Glu | Arg | Leu | Ala 235 | Asp | Ile | Lys | Ala | Ala 240 | |
| Ala | Gly | Ile | Pro | Glu 245 | Glu | Leu | Asp | Gly | Asp 250 | Val | Val | Thr | Val | Pro 255 | Lys | |
| Arg | Gly | Ser | Gly 260 | Asn | Glu | Lys | Arg | Val 265 | Trp | Lys | Glu | Leu | Ile 270 | Leu | Ser | |
| Pro | Thr | Pro 275 | Ala | Met | Arg | Arg | Ile 280 | Leu | Leu | Ser | Gly | Ile 285 | Gly | Ile | His | |
| Phe | Phe 290 | Gln | His | Ala | Leu | Gly 295 | Ile | His | Ser | Val | Val 300 | Phe | Tyr | Ser | Pro | |
| Leu 305 | Val | Phe | Lys | Ser | Pro 310 | Gly | Leu | Thr | Asn | Asp 315 | Lys | His | Phe | Leu | Gly 320 | |
| Thr | Thr | Trp | Pro | Phe 325 | Gly | Val | Thr | Lys | Arg 330 | Leu | Phe | Ile | Leu | Leu 335 | Ala | |
| Thr | Phe | Phe | Ile 340 | Asp | Gly | Val | Gly | Arg 345 | Arg | Pro | Leu | Leu | Leu 350 | Gly | Ser | |
| Thr | Gly | Gly 355 | Ile | Ile | Leu | Ser | Leu 360 | Ile | Gly | Leu | Gly | Ala 365 | Gly | Leu | Thr | |
| Val | Val 370 | Gly | Gln | His | Pro | Asp 375 | Ala | Lys | Ile | Pro | Trp 380 | Ala | Ile | Gly | Leu | |
| Ser 385 | Ile | Ala | Ser | Thr | Leu 390 | Ala | Tyr | Val | Ala | Phe 395 | Phe | Ser | Ile | Gly | Leu 400 | |
| Gly | Pro | Ile | Thr | Trp 405 | Val | Tyr | Ser | Ser | Glu 410 | Ile | Phe | Pro | Leu | Gln 415 | Val | |
| Arg | Ala | Leu | Gly 420 | Cys | Ser | Leu | Gly | Val 425 | Ala | Ala | Asn | Arg | Val 430 | Thr | Ser | |
| Gly | Val | Ile 435 | Ser | Met | Thr | Phe | Leu 440 | Ser | Leu | Ser | Lys | Ala 445 | Ile | Thr | Ile | |
| Gly | Gly 450 | Ser | Phe | Phe | Leu | Tyr 455 | Ser | Gly | Ile | Ala | Ala 460 | Leu | Ala | Trp | Val | |
| Phe | Phe | Tyr | Thr | Tyr | Leu | Pro | Glu | Thr | Arg | Gly | Arg | Thr | Leu | Glu | Glu | |

BB-1163 US DIV Correct Sequence Listing

465 470 475 480

Met Ser Lys Leu Phe Gly Asp Thr Ala Ala Ala Ser Glu Ser Asp Glu
485 490 495

Pro Ala Lys Glu Lys Lys Lys Val Glu Met Ala Ala Thr Asn
500 505 510

<210> 23
<211> 1853
<212> DNA
<213> Glycine max

<400> 23
gcacgagagt ttctctcttc acatatcatc atacttagat agtcagatac atcacccaat 60
aattaaatta aatacatgct agcacttta cagtactcct ttctctaata tctctctcat 120
attttccttt ctgcgatat tcagctaatt aaactaagtc actaagatga ctgagggaaa 180
gctagttgaa gctgcagaag ctcataagac acttcaggat ttcgatcctc caaagaagcg 240
caaaaggaac aagtatgctt ttgcttggtg tatgctggcc tccatgactt ccatcttgct 300
tggttatgat attggagtga tgagtggagc agccatatac ataaaaaggg acctgaaagt 360
ctcggacgag caaatcgaga tcctgctcgg aatcatcaac ctatactctc tgataggctc 420
atgtctcgcc ggcagaacct ccgactggat aggtccccgt tacacgattg ttttcgccgg 480
caccatcttc tttgtcggag cacttctcat gggtttctcc cccaattatt ctttctcat 540
gtttggccgt ttcgtcgtg gcattggcat cggctacgcc ctcatgatag ccccggtcta 600
caccgcccag gtctccccgg cctcctctcg tggcttcctc acttccttcc ctgaggtatt 660
tattaatgga gggatattaa ttggatacat atcaaactat gcattttcga agctgacact 720
aaaggtggga tggcgaatga tgcttgagat tgggtgcaata ctttcggtac tcctaacagt 780
aggagtgttg gcgatgccgg agtccccaa gtggcttggt atgaggggtc gtttgggaga 840
ggcaagaaaa gtgcttaaca aaacctcaga cagcaaggaa gaggcccaac taaggctagc 900
ggaaatcaaa caagccgcag ggatccccga gagttgcaac gacgacgtcg ttcaggtaaa 960
taaacaagc aacggtgaag gtgtatggaa agagctcttc ctctatccaa cgcccgaat 1020
tcgtcacatc gtaatcgctg cccttggtat tcacttcttc caacaagcgt cgggcgtaga 1080
cgccgtcgtt ttgtacagcc ccaggatctt cgaaaaggct gggattacaa acgacacgca 1140
taagcttctt gcaaccgtgg ccggttgatt cgtaagacc gtgttcatct tggcggctac 1200
gtttacgttg gaccgcgtgg gtcgtcgtcc gttgttattg tctagtgtcg gcggcatggt 1260
gctctcgtt ctcacgcttg cgatcagcct cactgttatt gatcattcgg agaggaaatt 1320
aatgtgggcc gttggatcga gcatagccat ggtgttggt tacgtggcca cgttctccat 1380
cggtgccggg cccatcacgt gggcttatag ttctgagatc ttcccgttga ggctgcgggc 1440
gcarggtgcg gccgcgggag ttgcggtgaa taggaccact agcgcggttg tctcaatgac 1500
ttttctgtcc ctactagag ccatactat tgggtggagct ttcttccttt attgtggcat 1560
tgctactgtt ggggtggatat tcttttacac cgtcttgctt gagacccggg gaaaaacgct 1620
cgaagacatg gaagggcttt ttggtacttt taggtccaaa tccaacgcca gcaaggctgt 1680
agaaaatgag aatgggcaag tagcacaagt ccagctagga accaatgtcc aaacttgaaa 1740
aatgagtatt gggacatcca gtaatagtga agtaatttcg tgattttttt tttgtttttt 1800
actttttaga ctagttcttc aaatcaaaac gagaagttaa agtgaaaaaa aaa 1853

<210> 24
<211> 523
<212> PRT
<213> Glycine max

<400> 24
Met Thr Glu Gly Lys Leu Val Glu Ala Ala Glu Ala His Lys Thr Leu
1 5 10 15
Gln Asp Phe Asp Pro Pro Lys Lys Arg Lys Arg Asn Lys Tyr Ala Phe
20 25 30
Ala Cys Ala Met Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp
35 40 45
Ile Gly Val Met Ser Gly Ala Ala Ile Tyr Ile Lys Arg Asp Leu Lys
50 55 60

BB-1163 US DIV Correct Sequence Listing

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Val 65 | Ser | Asp | Glu | Gln | Ile 70 | Glu | Ile | Leu | Leu | Gly 75 | Ile | Ile | Asn | Leu | Tyr 80 |
| Ser | Leu | Ile | Gly | Ser 85 | Cys | Leu | Ala | Gly | Arg 90 | Thr | Ser | Asp | Trp | Ile 95 | Gly |
| Pro | Arg | Tyr | Thr 100 | Ile | Val | Phe | Ala | Gly 105 | Thr | Ile | Phe | Phe | Val 110 | Gly | Ala |
| Leu | Leu | Met 115 | Gly | Phe | Ser | Pro | Asn 120 | Tyr | Ser | Phe | Leu | Met 125 | Phe | Gly | Arg |
| Phe | Val 130 | Ala | Gly | Ile | Gly | Ile 135 | Gly | Tyr | Ala | Leu | Met 140 | Ile | Ala | Pro | Val |
| Tyr 145 | Thr | Ala | Glu | Val | Ser 150 | Pro | Ala | Ser | Ser | Arg 155 | Gly | Phe | Leu | Thr | Ser 160 |
| Phe | Pro | Glu | Val | Phe 165 | Ile | Asn | Gly | Gly | Ile 170 | Leu | Ile | Gly | Tyr | Ile 175 | Ser |
| Asn | Tyr | Ala | Phe 180 | Ser | Lys | Leu | Thr | Leu 185 | Lys | Val | Gly | Trp | Arg 190 | Met | Met |
| Leu | Gly | Val 195 | Gly | Ala | Ile | Pro | Ser 200 | Val | Leu | Leu | Thr | Val 205 | Gly | Val | Leu |
| Ala | Met 210 | Pro | Glu | Ser | Pro | Arg 215 | Trp | Leu | Val | Met | Arg 220 | Gly | Arg | Leu | Gly |
| Glu 225 | Ala | Arg | Lys | Val | Leu 230 | Asn | Lys | Thr | Ser | Asp 235 | Ser | Lys | Glu | Glu | Ala 240 |
| Gln | Leu | Arg | Leu | Ala 245 | Glu | Ile | Lys | Gln | Ala 250 | Ala | Gly | Ile | Pro | Glu 255 | Ser |
| Cys | Asn | Asp | Asp 260 | Val | Val | Gln | Val | Asn 265 | Lys | Gln | Ser | Asn | Gly 270 | Glu | Gly |
| Val | Trp | Lys 275 | Glu | Leu | Phe | Leu | Tyr 280 | Pro | Thr | Pro | Ala | Ile 285 | Arg | His | Ile |
| Val | Ile 290 | Ala | Ala | Leu | Gly | Ile 295 | His | Phe | Phe | Gln | Gln 300 | Ala | Ser | Gly | Val |
| Asp 305 | Ala | Val | Val | Leu | Tyr 310 | Ser | Pro | Arg | Ile | Phe 315 | Glu | Lys | Ala | Gly | Ile 320 |
| Thr | Asn | Asp | Thr | His 325 | Lys | Leu | Leu | Ala | Thr 330 | Val | Ala | Val | Gly | Phe | Val 335 |
| Lys | Thr | Val | Phe 340 | Ile | Leu | Ala | Ala | Thr 345 | Phe | Thr | Leu | Asp | Arg 350 | Val | Gly |
| Arg | Arg | Pro 355 | Leu | Leu | Leu | Ser | Ser 360 | Val | Gly | Gly | Met | Val 365 | Leu | Ser | Leu |
| Leu | Thr 370 | Leu | Ala | Ile | Ser | Leu 375 | Thr | Val | Ile | Asp | His 380 | Ser | Glu | Arg | Lys |
| Leu 385 | Met | Trp | Ala | Val | Gly 390 | Ser | Ser | Ile | Ala | Met 395 | Val | Leu | Ala | Tyr | Val 400 |

BB-1163 US DIV Correct Sequence Listing

Ala Thr Phe Ser Ile Gly Ala Gly Pro Ile Thr Trp Val Tyr Ser Ser
405 410 415

Glu Ile Phe Pro Leu Arg Leu Arg Ala Gln Gly Ala Ala Ala Gly Val
420 425 430

Ala Val Asn Arg Thr Thr Ser Ala Val Val Ser Met Thr Phe Leu Ser
435 440 445

Leu Thr Arg Ala Ile Thr Ile Gly Gly Ala Phe Phe Leu Tyr Cys Gly
450 455 460

Ile Ala Thr Val Gly Trp Ile Phe Phe Tyr Thr Val Leu Pro Glu Thr
465 470 475 480

Arg Gly Lys Thr Leu Glu Asp Met Glu Gly Ser Phe Gly Thr Phe Arg
485 490 495

Ser Lys Ser Asn Ala Ser Lys Ala Val Glu Asn Glu Asn Gly Gln Val
500 505 510

Ala Gln Val Gln Leu Gly Thr Asn Val Gln Thr
515 520

<210> 25
<211> 2089
<212> DNA
<213> Triticum aestivum

<400> 25

| | | | | | | |
|------------|-------------|------------|-------------|------------|-------------|------|
| agcaccacta | aactatacac | aaggaggacc | tcgtcggcat | aatcctcagg | cagcgagcag | 60 |
| aggggcgctc | tcgacgatgg | accgcgccc | actcccggcg | gccgtcgagc | ccaagaagaa | 120 |
| gggcaacgtg | aggttcgcct | tcgcctgcgc | catcctcgcc | tccatgacct | ccatcctcct | 180 |
| cggctacgac | atcggcggtga | tgagcggagc | gtcgtgttac | atccagaagg | atctgaagat | 240 |
| caacgacacc | cagctggagg | tcctcatggg | catcctcaac | gtgtactcgc | tcattggctc | 300 |
| cttcgcggcg | gggcggacgt | ccgactggat | cggccggcg | ttcaccatcg | tcttcgccc | 360 |
| cgtcatcttc | ttcgcggg | ccctcatcat | gggcttctcc | gtcaactacg | ccatgctcat | 420 |
| gttcggg | ttcgtggccg | gcatcggcgt | ggggtacgct | ctcatgatcg | cggccgtgaa | 480 |
| cacggg | gtgtcccc | cgtctgccc | tggggttctc | acatccttcc | cggagggtgt | 540 |
| catcaacttc | ggcatcctcc | tcggatatgt | ctccaacttc | gccttcgccc | gcctctccct | 600 |
| ccgcctcggc | tggcgcat | tgctcggcat | aggcgcggtg | ccgtccgtcc | tgctcgcgtt | 660 |
| catggtgctc | ggcatgccc | agtctcccc | gtggctcgtc | atgaagggcc | gtctcgcgga | 720 |
| cggcaagggt | gtgcttgcca | agacgtccga | cacgccggaa | gaggccgccg | agcgcacgc | 780 |
| cgaattaag | actgccgccc | gcatccctct | gggcctcgac | ggcgacgtgg | tccccgtgcc | 840 |
| caaaaacaaa | ggaagcagcg | aggagaagcg | cgttttgaag | gacctcatcc | tgtcaccgac | 900 |
| catagccatg | cggcacatcc | tcatacgggg | aatcggcatc | cacttcttcc | agcagtcttc | 960 |
| gggcatcgac | gccgtcgtgc | tctacagccc | gctagttttc | aagagcgccg | gcatcacggg | 1020 |
| cgaagccgt | ctccgcggca | ccaccgtggc | ggtcggggcc | accaatacgg | tcttcatcct | 1080 |
| ggtggccacc | ttcctcctcg | accgcacccg | ccggcggccc | ctggtgctga | ccagcacggg | 1140 |
| cggcatgctc | gtctccttag | tgggcctcgc | gacggggctc | accgtcatca | gccgccaccc | 1200 |
| ggacgagaag | atcacctggg | ccatcgtcct | gtgcatcttc | tgcatcatgg | cctacgtggc | 1260 |
| cttcttctcc | atcggcctcg | gccccatcac | gtgggtgtac | agctcggaga | tcttcccgtc | 1320 |
| gcacgtgcgc | gcgctgggct | gctccctggg | cgtggccgct | aaccgcctga | ccagcggcgt | 1380 |
| gatctccatg | accttcattt | cgtgtgcca | ggccatgacc | atcggcggcg | ccttcttctc | 1440 |
| cttcgcgggc | atcgcctcat | tcgcatgggt | gttcttcttc | gcctacctgc | cggagacccg | 1500 |
| cggccgcacg | ctggaggaca | tgagctcgtc | gttcggcaac | acggccacgc | acaagcaggg | 1560 |
| cggcgcgga | gccgacgacg | acggcgggga | gaagaagggtg | gaaatggccg | ccaccaactg | 1620 |
| accgcaagtt | ggcagatcgc | gatgcgaaga | cttgcgctgt | atccgtctcg | gctagctagc | 1680 |
| tgccacaagg | ccacatagat | gacgaagtag | cgtgggaaga | ttcgtgatc | cggccggagc | 1740 |
| tgccggaggg | cgaaggcaag | ctccagctcg | atcgagacgt | taatggcttc | ttaaatgtgc | 1800 |
| taagtttaat | gtttcgtctc | ttggttttgt | ccgggtaggt | cgtgagcaat | ccggtagtgc | 1860 |
| cgatgccaa | gctaatacgac | gccggacgga | ctagactact | gtagtagact | gtagagggtgt | 1920 |

BB-1163 US DIV Correct Sequence Listing

accgttgcta cttccgtggc gtttgtctgc atgattagga gagaaaactg gcggtggttc 1980
gaggactcta cctgccgatc gagtgagtca agcgagccac ggaaaatgtg taagaaaaaa 2040
atattaagta tgtgtattgt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2089

<210> 26
<211> 539
<212> PRT
<213> Triticum aestivum

<400> 26
Ala Pro Leu Asn Tyr Thr Gln Gly Gly Pro Arg Arg His Asn Pro Gln
1 5 10 15
Ala Ala Ser Arg Gly Ala Ser Ser Thr Met Asp Arg Ala Ala Leu Pro
20 25 30
Ala Ala Val Glu Pro Lys Lys Lys Gly Asn Val Arg Phe Ala Phe Ala
35 40 45
Cys Ala Ile Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp Ile
50 55 60
Gly Val Met Ser Gly Ala Ser Leu Tyr Ile Gln Lys Asp Leu Lys Ile
65 70 75 80
Asn Asp Thr Gln Leu Glu Val Leu Met Gly Ile Leu Asn Val Tyr Ser
85 90 95
Leu Ile Gly Ser Phe Ala Ala Gly Arg Thr Ser Asp Trp Ile Gly Arg
100 105 110
Arg Phe Thr Ile Val Phe Ala Ala Val Ile Phe Phe Ala Gly Ala Leu
115 120 125
Ile Met Gly Phe Ser Val Asn Tyr Ala Met Leu Met Phe Gly Arg Phe
130 135 140
Val Ala Gly Ile Gly Val Gly Tyr Ala Leu Met Ile Ala Pro Val Asn
145 150 155 160
Thr Gly Glu Val Ser Pro Ala Ser Ala Arg Gly Val Leu Thr Ser Phe
165 170 175
Pro Glu Val Phe Ile Asn Phe Gly Ile Leu Leu Gly Tyr Val Ser Asn
180 185 190
Phe Ala Phe Ala Arg Leu Ser Leu Arg Leu Gly Trp Arg Ile Met Leu
195 200 205
Gly Ile Gly Ala Val Pro Ser Val Leu Leu Ala Phe Met Val Leu Gly
210 215 220
Met Pro Glu Ser Pro Arg Trp Leu Val Met Lys Gly Arg Leu Ala Asp
225 230 235 240
Ala Lys Val Val Leu Ala Lys Thr Ser Asp Thr Pro Glu Glu Ala Ala
245 250 255
Glu Arg Ile Ala Asp Ile Lys Thr Ala Ala Gly Ile Pro Leu Gly Leu
260 265 270
Asp Gly Asp Val Val Pro Val Pro Lys Asn Lys Gly Ser Ser Glu Glu
275 280 285

BB-1163 US DIV Correct Sequence Listing

Lys Arg Val Leu Lys Asp Leu Ile Leu Ser Pro Thr Ile Ala Met Arg
 290 295 300
 His Ile Leu Ile Ala Gly Ile Gly Ile His Phe Phe Gln Gln Ser Ser
 305 310 315 320
 Gly Ile Asp Ala Val Val Leu Tyr Ser Pro Leu Val Phe Lys Ser Ala
 325 330 335
 Gly Ile Thr Gly Asp Ser Arg Leu Arg Gly Thr Thr Val Ala Val Gly
 340 345 350
 Ala Thr Asn Thr Val Phe Ile Leu Val Ala Thr Phe Leu Leu Asp Arg
 355 360 365
 Ile Arg Arg Arg Pro Leu Val Leu Thr Ser Thr Gly Gly Met Leu Val
 370 375 380
 Ser Leu Val Gly Leu Ala Thr Gly Leu Thr Val Ile Ser Arg His Pro
 385 390 395 400
 Asp Glu Lys Ile Thr Trp Ala Ile Val Leu Cys Ile Phe Cys Ile Met
 405 410 415
 Ala Tyr Val Ala Phe Phe Ser Ile Gly Leu Gly Pro Ile Thr Trp Val
 420 425 430
 Tyr Ser Ser Glu Ile Phe Pro Leu His Val Arg Ala Leu Gly Cys Ser
 435 440 445
 Leu Gly Val Ala Val Asn Arg Leu Thr Ser Gly Val Ile Ser Met Thr
 450 455 460
 Phe Ile Ser Leu Ser Lys Ala Met Thr Ile Gly Gly Ala Phe Phe Leu
 465 470 475 480
 Phe Ala Gly Ile Ala Ser Phe Ala Trp Val Phe Phe Phe Ala Tyr Leu
 485 490 495
 Pro Glu Thr Arg Gly Arg Thr Leu Glu Asp Met Ser Ser Leu Phe Gly
 500 505 510
 Asn Thr Ala Thr His Lys Gln Gly Ala Ala Glu Ala Asp Asp Asp Ala
 515 520 525
 Gly Glu Lys Lys Val Glu Met Ala Ala Thr Asn
 530 535

<210> 27
 <211> 1872
 <212> DNA
 <213> Triticum aestivum

<400> 27
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 gcagatgaaa atgtctccgg aaagaaaagg agcggaggac aaggaagaag gatcgaggat 120
 ggcttctgct gcgctcccgg agccgggggc agtccatcca aggaacaagg gcaatttcaa 180
 gtacgccttc acctgcgccc tctgtgcttc catggccacc atcgtcctcg gctacgacgt 240
 tggggtgatg agcgggtgct cgctgtacat caagagggac ctgcagatca cggacgtgca 300
 gctggagatc atgatgggca tcctgagcgt gtacgcgctc atcgggtcct tcctcggcgc 360
 gaggacgtcc gactgggtcg gccgccgcgt caccgtcgtc ttcgcggccg ccattctcaa 420
 caacggctcc ttgctcatgg gcttcgcggt caactacgcc atgctcatgg tcgggcgctt 480

BB-1163 US DIV Correct Sequence Listing

```

cgtcaccgga atcggcgtgg gctacgccat catggtcgcg ccagtgtaca cgcccagagt 540
gtccccggcg tcggcccgcg gcttcctcac gtctttcacc gaggtgttca tcaatgtggg 600
catcctcctt ggctacgtct ccaactacgc cttcgcgcgc ctcccgctcc acctcagctg 660
gcgcgtcatg ctcggcatcg gcgccgtccc gtccgccctg cttgcgctca tgggtgttcg 720
catgccggag tctcctcgct ggctcgtcat gaaaggccgc ctcgcggacg ccagggccgt 780
tctggccaag acctccgaca cgccggagga ggccgtggag cgccttgacc agatcaaggc 840
tgccgcccgc atccctaggg aacttgacgg cgacgtgggc gtcatgccta agacaaaagg 900
cggccaggag aagcaggtgt ggaaggagct catcttttcg ccgaccccag ccatgcggcg 960
catactgctc gcggcgctcg gcatccattt ctttcagcag gcgacgggct ccgactccgt 1020
cgtgctctat agcccacgcg tggtccagag cgcgggcatc accggcgaca accacctgct 1080
cggcgccaca tgcgccatgg gggtcgatga gacgctcttc atcctgggtg ccacgttcca 1140
gctcgaccgc gtcggcaggc ggccgctgct gctgaccagc acggccggca tgctcgctg 1200
tctcatcggc ctcgggacgg gcctcaccgt cgtgggtcgg caccggacg ccaaggtccc 1260
gtggggccatc ggcctgtgca tcgtgtccat cttggcctac gtgtccttct tctccatcgg 1320
cctcgggccc ctcaccagcg tgtacacctc ggaggtcttc ccactgcggg tgcgcgcgct 1380
gggcttcgcy ctgggcacgt catgcaaccg cgtcaccagc gccgcggtct ccatgtcctt 1440
cctgtccttg tccaaggcca tcaccatcgg cggcagcttc ttcctgtacg ccggcatcgc 1500
ggcgatagga tggattttct tcttcacctt cattccggag acgcgtggcc tgccgctcga 1560
ggagataggg aagcttttcg gcatgacgga cacggccgtc gaagcccaag acaccgccac 1620
gaaagacaag gcgaaagtag gggagatgaa ctagtgaagt agacgtcaac caactgttac 1680
cgatgtacta ccatagagat gtatctgatc aacgtggcaa tataagtgtc acggactctt 1740
ggtgctcatt gatggattgt ttggataaaa tttcaagaga attgtttcaa gtttgatcc 1800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1860
aaaaaaaaaa aa 1872

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<210> 28
 <211> 529
 <212> PRT
 <213> Triticum aestivum

<400> 28
 Met Lys Met Ser Pro Glu Arg Lys Gly Ala Glu Asp Lys Glu Glu Gly
 1 5 10 15
 Ser Arg Met Ala Ser Ala Ala Leu Pro Glu Pro Gly Ala Val His Pro
 20 25 30
 Arg Asn Lys Gly Asn Phe Lys Tyr Ala Phe Thr Cys Ala Leu Cys Ala
 35 40 45
 Ser Met Ala Thr Ile Val Leu Gly Tyr Asp Val Gly Val Met Ser Gly
 50 55 60
 Ala Ser Leu Tyr Ile Lys Arg Asp Leu Gln Ile Thr Asp Val Gln Leu
 65 70 75 80
 Glu Ile Met Met Gly Ile Leu Ser Val Tyr Ala Leu Ile Gly Ser Phe
 85 90 95
 Leu Gly Ala Arg Thr Ser Asp Trp Val Gly Arg Arg Val Thr Val Val
 100 105 110
 Phe Ala Ala Ala Ile Phe Asn Asn Gly Ser Leu Leu Met Gly Phe Ala
 115 120 125
 Val Asn Tyr Ala Met Leu Met Val Gly Arg Phe Val Thr Gly Ile Gly
 130 135 140
 Val Gly Tyr Ala Ile Met Val Ala Pro Val Tyr Thr Pro Glu Val Ser
 145 150 155 160
 Pro Ala Ser Ala Arg Gly Phe Leu Thr Ser Phe Thr Glu Val Phe Ile
 165 170 175

BB-1163 US DIV Correct Sequence Listing

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Gly | Ile | Leu | Leu | Gly | Tyr | Val | Ser | Asn | Tyr | Ala | Phe | Ala | Arg |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Pro | Leu | His | Leu | Ser | Trp | Arg | Val | Met | Leu | Gly | Ile | Gly | Ala | Val |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Pro | Ser | Ala | Leu | Leu | Ala | Leu | Met | Val | Phe | Gly | Met | Pro | Glu | Ser | Pro |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Arg | Trp | Leu | Val | Met | Lys | Gly | Arg | Leu | Ala | Asp | Ala | Arg | Ala | Val | Leu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ala | Lys | Thr | Ser | Asp | Thr | Pro | Glu | Glu | Ala | Val | Glu | Arg | Leu | Asp | Gln |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ile | Lys | Ala | Ala | Ala | Gly | Ile | Pro | Arg | Glu | Leu | Asp | Gly | Asp | Val | Val |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Val | Met | Pro | Lys | Thr | Lys | Gly | Gly | Gln | Glu | Lys | Gln | Val | Trp | Lys | Glu |
| | | 275 | | | | 280 | | | | | | 285 | | | |
| Leu | Ile | Phe | Ser | Pro | Thr | Pro | Ala | Met | Arg | Arg | Ile | Leu | Leu | Ala | Ala |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Leu | Gly | Ile | His | Phe | Phe | Gln | Gln | Ala | Thr | Gly | Ser | Asp | Ser | Val | Val |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Leu | Tyr | Ser | Pro | Arg | Val | Phe | Gln | Ser | Ala | Gly | Ile | Thr | Gly | Asp | Asn |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| His | Leu | Leu | Gly | Ala | Thr | Cys | Ala | Met | Gly | Val | Met | Lys | Thr | Leu | Phe |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Ile | Leu | Val | Ala | Thr | Phe | Gln | Leu | Asp | Arg | Val | Gly | Arg | Arg | Pro | Leu |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Leu | Leu | Thr | Ser | Thr | Ala | Gly | Met | Leu | Ala | Cys | Leu | Ile | Gly | Leu | Gly |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Thr | Gly | Leu | Thr | Val | Val | Gly | Arg | His | Pro | Asp | Ala | Lys | Val | Pro | Trp |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ala | Ile | Gly | Leu | Cys | Ile | Val | Ser | Ile | Leu | Ala | Tyr | Val | Ser | Phe | Phe |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Ser | Ile | Gly | Leu | Gly | Pro | Leu | Thr | Ser | Val | Tyr | Thr | Ser | Glu | Val | Phe |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Pro | Leu | Arg | Val | Arg | Ala | Leu | Gly | Phe | Ala | Leu | Gly | Thr | Ser | Cys | Asn |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Arg | Val | Thr | Ser | Ala | Ala | Val | Ser | Met | Ser | Phe | Leu | Ser | Leu | Ser | Lys |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Ala | Ile | Thr | Ile | Gly | Gly | Ser | Phe | Phe | Leu | Tyr | Ala | Gly | Ile | Ala | Ala |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Ile | Gly | Trp | Ile | Phe | Phe | Phe | Thr | Phe | Ile | Pro | Glu | Thr | Arg | Gly | Leu |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| Pro | Leu | Glu | Glu | Ile | Gly | Lys | Leu | Phe | Gly | Met | Thr | Asp | Thr | Ala | Val |
| | | | 500 | | | | | 505 | | | | | 510 | | |

BB-1163 US DIV Correct Sequence Listing

Glu Ala Gln Asp Thr Ala Thr Lys Asp Lys Ala Lys Val Gly Glu Met
515 520 525

Asn

<210> 29
<211> 729
<212> PRT
<213> Arabidopsis thaliana

<400> 29
Met Ser Gly Ala Val Leu Val Ala Ile Ala Ala Ala Val Gly Asn Leu
1 5 10 15
Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val Leu Tyr Ile
20 25 30
Lys Lys Glu Phe Asn Leu Glu Ser Asn Pro Ser Val Glu Gly Leu Ile
35 40 45
Val Ala Met Ser Leu Ile Gly Ala Thr Leu Ile Thr Thr Cys Ser Gly
50 55 60
Gly Val Ala Asp Trp Leu Gly Arg Arg Pro Met Leu Ile Leu Ser Ser
65 70 75 80
Ile Leu Tyr Phe Val Gly Ser Leu Val Met Leu Trp Ser Pro Asn Val
85 90 95
Tyr Val Leu Leu Leu Gly Arg Leu Leu Asp Gly Phe Gly Val Gly Leu
100 105 110
Val Val Thr Leu Val Pro Ile Tyr Ile Ser Glu Thr Ala Pro Pro Glu
115 120 125
Ile Arg Gly Leu Leu Asn Thr Leu Pro Gln Phe Thr Gly Ser Gly Gly
130 135 140
Met Phe Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Met Pro Ser
145 150 155 160
Pro Ser Trp Arg Leu Met Leu Gly Val Leu Phe Ile Pro Ser Leu Val
165 170 175
Phe Phe Phe Leu Thr Val Phe Phe Leu Pro Glu Ser Pro Arg Trp Leu
180 185 190
Val Ser Lys Gly Arg Met Leu Glu Ala Lys Arg Val Leu Gln Arg Leu
195 200 205
Arg Gly Arg Glu Asp Val Ser Gly Glu Met Ala Leu Leu Val Glu Gly
210 215 220
Leu Gly Ile Gly Gly Glu Thr Thr Ile Glu Glu Tyr Ile Ile Gly Pro
225 230 235 240
Ala Asp Glu Val Thr Asp Asp His Asp Ile Ala Val Asp Lys Asp Gln
245 250 255
Ile Lys Leu Tyr Gly Ala Glu Glu Gly Leu Ser Trp Val Ala Arg Pro
260 265 270

BB-1163 US DIV Correct Sequence Listing

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Gly | Gly | Ser | Thr | Met | Ser | Val | Leu | Ser | Arg | His | Gly | Ser | Thr |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Met | Ser | Arg | Arg | Gln | Gly | Ser | Leu | Ile | Asp | Pro | Leu | Val | Thr | Leu | Phe |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Gly | Ser | Val | His | Glu | Lys | Met | Pro | Asp | Thr | Gly | Ser | Met | Arg | Ser | Ala |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Leu | Phe | Pro | His | Phe | Gly | Ser | Met | Phe | Ser | Val | Gly | Gly | Asn | Gln | Pro |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Arg | His | Glu | Asp | Trp | Asp | Glu | Glu | Asn | Leu | Val | Gly | Glu | Gly | Glu | Asp |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Tyr | Pro | Ser | Asp | His | Gly | Asp | Asp | Ser | Glu | Asp | Asp | Leu | His | Ser | Pro |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Leu | Ile | Ser | Arg | Gln | Thr | Thr | Ser | Met | Glu | Lys | Asp | Met | Pro | His | Thr |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Ala | His | Gly | Thr | Leu | Ser | Thr | Phe | Arg | His | Gly | Ser | Gln | Val | Gln | Gly |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ala | Gln | Gly | Glu | Gly | Ala | Gly | Ser | Met | Gly | Ile | Gly | Gly | Gly | Trp | Gln |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Val | Ala | Trp | Lys | Trp | Thr | Glu | Arg | Glu | Asp | Glu | Ser | Gly | Gln | Lys | Glu |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Glu | Gly | Phe | Pro | Gly | Ser | Arg | Arg | Gly | Ser | Ile | Val | Ser | Leu | Pro | Gly |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Gly | Asp | Gly | Thr | Gly | Glu | Ala | Asp | Phe | Val | Gln | Ala | Ser | Ala | Leu | Val |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Ser | Gln | Pro | Ala | Leu | Tyr | Ser | Lys | Asp | Leu | Leu | Lys | Glu | His | Thr | Ile |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Gly | Pro | Ala | Met | Val | His | Pro | Ser | Glu | Thr | Thr | Lys | Gly | Ser | Ile | Trp |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| His | Asp | Leu | His | Asp | Pro | Gly | Val | Lys | Arg | Ala | Leu | Val | Val | Gly | Val |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Gly | Leu | Gln | Ile | Leu | Gln | Gln | Phe | Ser | Gly | Ile | Asn | Gly | Val | Leu | Tyr |
| | | 515 | | | | | 520 | | | | | 525 | | | |
| Tyr | Thr | Pro | Gln | Ile | Leu | Glu | Gln | Ala | Gly | Val | Gly | Ile | Leu | Leu | Ser |
| | 530 | | | | | 535 | | | | | 540 | | | | |
| Asn | Met | Gly | Ile | Ser | Ser | Ser | Ser | Ala | Ser | Leu | Leu | Ile | Ser | Ala | Leu |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Thr | Thr | Phe | Val | Met | Leu | Pro | Ala | Ile | Ala | Val | Ala | Met | Arg | Leu | Met |
| | | | | 565 | | | | | 570 | | | | | 575 | |
| Asp | Leu | Ser | Gly | Arg | Arg | Thr | Leu | Leu | Leu | Thr | Thr | Ile | Pro | Ile | Leu |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Ile | Ala | Ser | Leu | Leu | Val | Leu | Val | Ile | Ser | Asn | Leu | Val | His | Met | Asn |
| | | 595 | | | | | 600 | | | | | 605 | | | |

BB-1163 US DIV Correct Sequence Listing

Ser Ile Val His Ala Val Leu Ser Thr Val Ser Val Val Leu Tyr Phe
610 615 620
Cys Phe Phe Val Met Gly Phe Gly Pro Ala Pro Asn Ile Leu Cys Ser
625 630 635 640
Glu Ile Phe Pro Thr Arg Val Arg Gly Ile Cys Ile Ala Ile Cys Ala
645 650 655
Leu Thr Phe Trp Ile Cys Asp Ile Ile Val Thr Tyr Ser Leu Pro Val
660 665 670
Leu Leu Lys Ser Ile Gly Leu Ala Gly Val Phe Gly Met Tyr Ala Ile
675 680 685
Val Cys Cys Ile Ser Trp Val Phe Val Phe Ile Lys Val Pro Glu Thr
690 695 700
Lys Gly Met Pro Leu Glu Val Ile Thr Glu Phe Phe Ser Val Gly Ala
705 710 715 720
Arg Gln Ala Glu Ala Lys Asn Glu
725

<210> 30
<211> 549
<212> PRT
<213> Beta vulgaris

<400> 30
Met Ser Glu Gly Thr Asn Lys Ala Met Ser Asp Pro Pro Pro Thr Thr
1 5 10 15
Ala Ser Lys Val Ile Ala Asp Phe Asp Pro Leu Lys Lys Pro Pro Lys
20 25 30
Arg Asn Lys Phe Ala Phe Ala Cys Ala Thr Leu Ala Ser Met Thr Ser
35 40 45
Val Leu Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala Ile Ile Tyr
50 55 60
Leu Lys Glu Asp Trp His Ile Ser Asp Thr Gln Ile Gly Val Leu Val
65 70 75 80
Gly Ile Leu Asn Ile Tyr Cys Leu Phe Gly Ser Phe Ala Ala Gly Arg
85 90 95
Thr Ser Asp Trp Ile Gly Arg Arg Tyr Thr Ile Val Leu Ala Gly Ala
100 105 110
Ile Phe Phe Val Gly Ala Leu Leu Met Gly Phe Ala Thr Asn Tyr Ala
115 120 125
Phe Leu Met Val Gly Arg Phe Val Thr Gly Ile Gly Val Gly Tyr Ala
130 135 140
Leu Met Ile Ala Pro Val Tyr Thr Ala Glu Val Ser Pro Ala Ser Ser
145 150 155 160
Arg Gly Phe Leu Thr Ser Phe Pro Glu Val Phe Ile Asn Ala Gly Ile
165 170 175

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Gly | Tyr | Ile | Ser | Asn | Leu | Ala | Phe | Ser | Ser | Leu | Pro | Thr | His |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Ser | Trp | Arg | Phe | Met | Leu | Gly | Ile | Gly | Ala | Ile | Pro | Ser | Ile | Phe |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Leu | Ala | Ile | Gly | Val | Leu | Ala | Met | Pro | Glu | Ser | Pro | Arg | Trp | Leu | Val |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Met | Gln | Gly | Arg | Leu | Gly | Asp | Ala | Lys | Lys | Val | Leu | Asn | Arg | Ile | Ser |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Asp | Ser | Pro | Glu | Glu | Ala | Gln | Leu | Arg | Leu | Ser | Glu | Ile | Lys | Gln | Thr |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ala | Gly | Ile | Pro | Ala | Glu | Cys | Asp | Glu | Asp | Ile | Tyr | Lys | Val | Glu | Lys |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Thr | Lys | Ile | Lys | Ser | Gly | Asn | Ala | Val | Trp | Lys | Glu | Leu | Phe | Phe | Asn |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Pro | Thr | Pro | Ala | Val | Arg | Arg | Ala | Val | Ile | Ala | Gly | Ile | Gly | Ile | His |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Phe | Phe | Gln | Gln | Ala | Ser | Gly | Ile | Asp | Ala | Val | Val | Leu | Tyr | Ser | Pro |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Arg | Ile | Phe | Gln | Ser | Ala | Gly | Ile | Thr | Asn | Ala | Arg | Lys | Gln | Leu | Leu |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Ala | Thr | Val | Ala | Val | Gly | Val | Val | Lys | Thr | Leu | Phe | Ile | Leu | Val | Ala |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Thr | Phe | Gln | Leu | Asp | Lys | Tyr | Gly | Arg | Arg | Pro | Leu | Leu | Leu | Thr | Ser |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Val | Gly | Gly | Met | Ile | Ile | Ala | Ile | Leu | Thr | Leu | Ala | Met | Ser | Leu | Thr |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Val | Ile | Asp | His | Ser | His | His | Lys | Ile | Thr | Trp | Ala | Ile | Ala | Leu | Cys |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ile | Thr | Met | Val | Cys | Ala | Val | Val | Ala | Ser | Phe | Ser | Ile | Gly | Leu | Gly |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Pro | Ile | Thr | Trp | Val | Tyr | Ser | Ser | Glu | Val | Phe | Pro | Leu | Arg | Leu | Arg |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Ala | Gln | Gly | Thr | Ser | Met | Gly | Val | Ala | Val | Asn | Arg | Val | Val | Ser | Gly |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Val | Ile | Ser | Ile | Phe | Phe | Leu | Pro | Leu | Ser | His | Lys | Ile | Thr | Thr | Gly |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Gly | Ala | Phe | Phe | Leu | Phe | Gly | Gly | Ile | Ala | Ile | Ile | Ala | Trp | Phe | Phe |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Phe | Leu | Thr | Phe | Leu | Pro | Glu | Thr | Arg | Gly | Arg | Thr | Leu | Glu | Asn | Met |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| His | Glu | Leu | Phe | Glu | Asp | Phe | Arg | Trp | Arg | Glu | Ser | Phe | Pro | Gly | Asn |
| | | | 500 | | | | | 505 | | | | | 510 | | |

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Lys Ser Asn Asn Asp Glu Asn Ser Thr Arg Lys Gln Ser Asn Gly Asn
515 520 525

Asp Lys Ser Gln Val Gln Leu Gly Glu Thr Thr Thr Ser Thr Thr Val
530 535 540

Thr Asn Asp Asn His
545